

# *Aeromonas hydrophila* Flagella Glycosylation: Involvement of a Lipid Carrier

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## Abstract

Polar flagellin proteins from *Aeromonas hydrophila* strain AH-3 (serotype O34) were found to be O-glycosylated with a heterogeneous glycan. Mutants unable to produce WecP or Gne enzymes showed altered motility, and the study of their polar flagellin glycosylation showed that the patterns of glycosylation differed from that observed with wild type polar flagellin. This suggested the involvement of a lipid carrier in glycosylation. A gene coding for an enzyme linking sugar to a lipid carrier was identified in strain AH-3 (WecX) and subsequent mutation abolished completely motility, flagella production by EM, and flagellin glycosylation. This is the first report of a lipid carrier involved in flagella O-glycosylation. A molecular model has been proposed. The results obtained suggested that the N-acetylhexosamines are N-acetylgalactosamines and that the heptasaccharide is completely independent of the O34-antigen lipopolysaccharide. Furthermore, by comparing the mutants with differing degrees of polar flagellin glycosylation, we established their importance in *A. hydrophila* flagella formation and motility.

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## Introduction

Mesophilic *Aeromonas* are ubiquitous water-borne bacteria, considered opportunistic pathogens of both aquatic and terrestrial animals, some species being associated with gastrointestinal and extraintestinal human diseases [1]. These bacteria constitutively express a single polar flagellum, although about 60% of strains most commonly associated with diarrhoea [2] are also able to express many lateral flagella when grown in viscous environments or on surfaces [3]. Investigations have revealed that both the polar and lateral flagella systems of the mesophilic *Aeromonas* are involved in adherence to both biotic and abiotic surfaces, as well as in biofilm formation [4]. Flagella motility in *Aeromonas*, like in other motile bacteria, represents an important advantage in moving towards favourable conditions or in avoiding detrimental environments and it allows the bacterium to successfully compete with other microorganisms [5]. *A. hydrophila* flagella morphogenesis, as happens in other motile Gram-negative bacteria, is a complex cascade of events that requires coordinated expression of more than 50 genes encoding structural subunits, regulatory proteins and chemo-sensor machinery.

Glycosylation, either N or O linked, is increasingly being observed in bacteria reviewed in [6–8], with the most commonly reported bacterial glycoproteins being flagellins and pili. *Campylobacter jejuni* is a bacterium with a well-characterized N-glycosylation general pathway with a heptasaccharide built through a lipid carrier undecaprenyl phosphate (Und-P) [7]. In addition to this

general protein glycosylation pathway *C. jejuni* also shows O-linked glycans modifying their flagellins, however with more simple glycans never built through Und-P [7]. A similar situation is observed in *Helicobacter pylori* [7].

Frequently, the linkage of the glycan to the proteins is an O-linkage of the sugar moiety to the hydroxyl oxygen of serine (Ser) or threonine (Thr) residues of proteins [6]. This is usually catalysed through glycosyltransferases and the need for a lipid carrier for O-glycosylation of proteins is rare. We recently demonstrated that polar and lateral flagellin proteins from *Aeromonas hydrophila* strain AH-3 (serotype O34) are glycosylated with different carbohydrate moieties [9]. The lateral flagellin is modified at three sites in O-linkage, with a single monosaccharide shown to be a pseudaminic acid derivative of 376 Da. The polar flagellin is modified with a heterogeneous glycan, comprised of a heptasaccharide of, the 376 Da pseudaminic acid type sugar, two hexoses, three N-acetylhexosamines, and an unknown glycan of 102 Da. This glycan chain is linked through the 376 Da sugar to the protein backbone, also in O-linkage. Furthermore, deletion of several genes within the putative pseudaminic acid biosynthetic locus, resulted in abolition of polar and lateral flagella formation by posttranscriptional regulation of the flagellins. In our prior work we were not able to determine the mechanism by which the heptasaccharide chain was formed, or the biological role of flagellin glycosylation. No flagellin until now has been shown to be modified by a glycan built up through Und-P, or showing a complicated glycan structure like the one described previously on *A. hydrophila* AH-3 [9]. The

involvement of a lipid carrier in bacterial protein glycosylation has been only described in fimbriae glycosylation from *Neisseria* and *Pseudomonas* [10–12].

Surface bacterial polysaccharides, such as O-antigen lipopolysaccharides, capsules or cell wall peptidoglycans, are synthesised in the cytoplasm and subsequently translocated to their location on the bacterial surface. Despite the heterogeneity in the different surface carbohydrates, biosynthesis is commonly initiated with an integral membrane protein that catalyzes the transfer of glucose (Glc)/galactose (Gal)-1-phosphate (WbaP) or *N*-acetylhexosamine (GlcNAc or GalNAc)-1-phosphate (WecA or WecP, respectively) onto the Und-P [13,14]. These enzymes have multiple transmembrane helices, and the cytosolic loops contribute to form a catalytic site [15]. The predicted topology of these enzymes is variable and linked to their substrate specificity in different cases, like WbaP, WecA or WecP [16–18].

In the current study we demonstrated that a lipid carrier is involved in the heptasaccharide *O*-glycosylation of polar flagellins in strain AH-3. We showed that the HexNAc from the polar flagellin glycan is *N*-acetyl galactosamine (GalNAc) or a derivative of it. In addition we begin to shed light on the biological role of flagellin glycosylation with data linking flagellin glycosylation to motility.

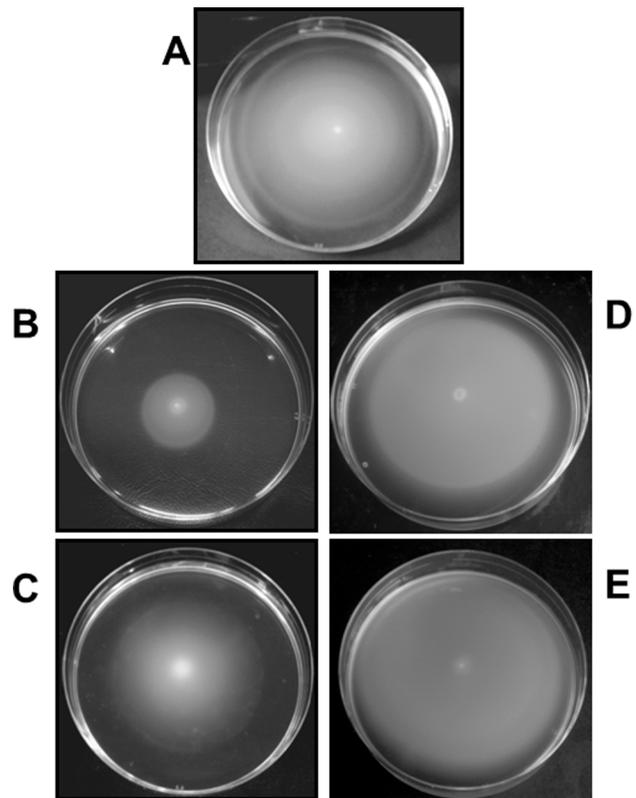
## Results

Our previous work has shown *A. hydrophila* AH-3 flagellins to be post-translationally modified with glycan moieties [9]. The lateral flagellin was observed to be glycosylated with a unique 376 Da sugar residue, a putative pseudaminic acid derivative. In contrast, the polar flagellin was modified with a heptasaccharide glycan, comprised of three *N*-acetylhexosamines additionally modified by variable numbers of phosphate groups and methyl groups, two hexoses and two unknown glycans of 376 Da (putative pseudaminic acid derivative) and 102 Da. This gave a monosaccharide mass sequence of 376-162-162-203-296-376-102 Da.

The aim of the current study is to understand the mechanisms of the differential glycosylation of polar and lateral flagellins using two previously isolated motility deficient mutants from this strain: a *wecP* mutant (AH-3Δ*WecP*) and a *gne* mutant (AH-2767). *WecP* is the enzyme codified by a gene in the O34-antigen LPS cluster linking UDP-GalNAc to the Und-P [6], while *Gne* is the enzyme able to 4-epimerize UDP-GlcNAc to UDP-GalNAc [19] codified outside the O34-antigen LPS cluster by a gene alone between non related genes codifying for a ferredoxin oxidoreductase and a protein-disulfide isomerase. We have previously shown that both mutants are devoid of the O34-antigen LPS [18,19].

### *A. hydrophila* AH-3 *wecP* Mutant (AH-3Δ*WecP*)

This mutant is able to produce both polar and lateral flagella. No differences were observed between the wild type strain and the AH-3Δ*WecP* mutant in lateral flagella production grown on solid or semisolid media when examined by EM. However, the AH-3Δ*WecP* mutant showed a reduction in motility compared to the wild type strain when assayed on swim agar plates (Figure 1). This motility reduction was confirmed by light microscopy observations in liquid media. This fact prompted us to purify the polar flagellum and compare it to the wild type. A reduction in the molecular weight of AH-3Δ*WecP* polar flagellins, was observed by SDS-PAGE, as shown in Figure 2A. The amount of polar flagellin obtained from 1 l culture of the mutant versus the same amount of wild type growth is reduced in approximately 50% judged by protein concentration analysis.



**Figure 1. Motility phenotypes exhibited in swim (0.25%) agar by *A. hydrophila* AH-3 (A), AH-2767 *gne* mutant (B), AH-3Δ*WecP* mutant (C), AH-2767+ pACYC-Gne (D), and AH-3Δ*WecP* pBAD-WecP (E).**

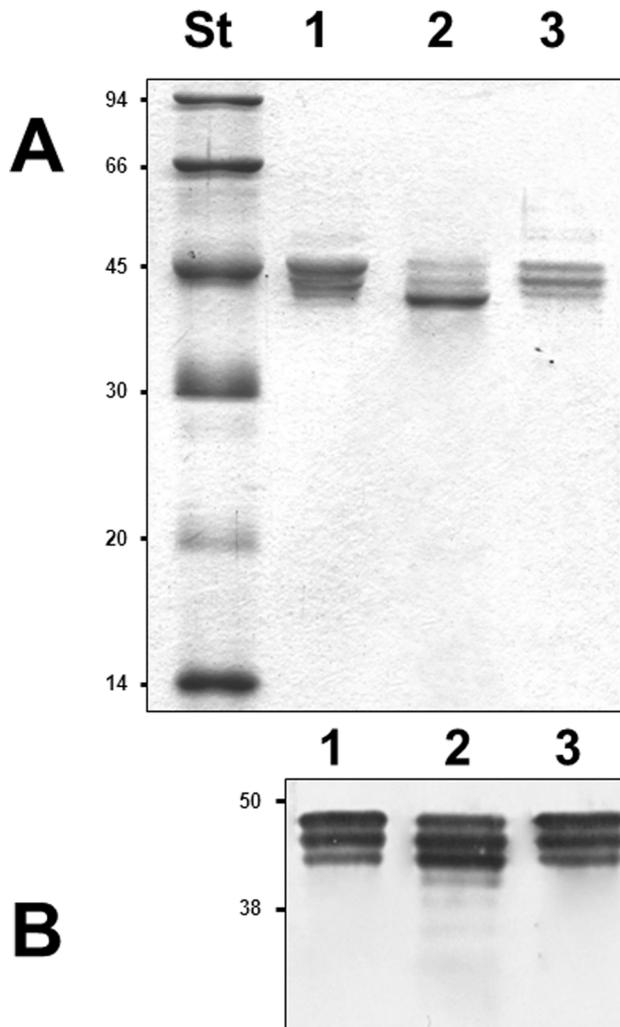
doi:10.1371/journal.pone.0089630.g001

A full recovery of all the reduced characteristics observed in the AH-3Δ*WecP* mutant versus the wild type (motility or molecular weight reduction and variation of polar flagellins) were achieved when we introduced pBAD33-*WecP*<sub>Ah</sub> plasmid [18] (Figure 1 and 2). No changes were observed when we introduced the plasmid vector alone in the same mutant.

### Mass Spectrometry Analysis of Polar Flagellin from an *A. hydrophila* AH-3 *WecP* Mutant

Protein mass analysis was carried out by using electrospray ionisation mass spectrometry on polar flagellins isolated from the AH-3Δ*WecP* mutant. Although poor ionisation prevented spectral deconvolution, and the observed protein masses were not determined.

MS/MS analyses of tryptic peptides from polar flagellins isolated from the AH-3Δ*WecP* mutant showed the same peptides to be modified with glycan as the wild type strain (Table 1), however differences in the glycan modification were observed. To highlight the observed differences in glycopeptide profiles observed between AH-3Δ*WecP* mutant and wild type, Figure 3 shows alignment of LC-MS spectra from tryptic digests of polar flagellin isolated from wild type (Figure 3a) and AH-3Δ*WecP* mutant (Figure 3b) at 13.1–13.8 minutes (elution time for the <sup>94–109</sup>TLAQQSANGSN NTDDR glycopeptide). In our previous study, we reported the glycopeptides to be observed in LC-MS spectra as clusters of multiple charged ions. These clusters of ions corresponded to the glycan heterogeneity. In Figure 3a, these clusters are denoted 1–4 and correspond to different amounts of



**Figure 2. Purified polar flagellins from several *A. hydrophila* strains obtained according to Materials and Methods.** A/SDS-PAGE and B/Western blot using specific antiserum against purified polar flagellins. St, size standard (14, 20, 30, 45, 60, and 94 kDa). 1, *A. hydrophila* AH-3 (wild type); 2, *A. hydrophila* AH-3ΔWecP mutant and 3, *A. hydrophila* AH-3ΔWecP complemented with plasmid pBAD33-WecP<sub>Ah</sub> (18). Figure 2A lane 2 shows a clear reduction in the AH-3ΔWecP mutant polar flagellin MW. In Figure 2B the AH-3ΔWecP mutant polar flagellin shows several minor bands with reduced MW (lane 2) not observed neither in lane 1 (wild type) or lane 3 (complemented mutant). doi:10.1371/journal.pone.0089630.g002

phosphorylation or methylation of the sugars comprising the heptasaccharide chains. When comparing the LC-MS spectra of wild type and WecP mutant, it is notable that the relative abundance of the glycopeptide isoforms differs between the mutant and wild type strain. In particular, the most abundant form of the <sup>94–109</sup>TLAQQSANGSNNTDDR glycopeptide in the AH-3ΔWecP mutant is modified with single pseudaminic acid type modification (doubly charged ion observed at  $m/z$  1034.4, indicated in Figure 3a and b with an arrow). The glycopeptides harbouring the variable heptasaccharide glycan modifications, denoted clusters 1–4, were observed in the LC-MS spectrum, at much lower intensity when compared with wild type glycopeptide clusters (Figure 3b). In particular, the prominent triply charged glycopeptides at  $m/z$  1062.1, 1089.4, 1120.4, 1151.4 were

observed in both wild type and AH-3ΔWecP mutant (in ion clusters 1–4). These ions correspond to the <sup>94–109</sup>TLAQQSANGSNNTDDR peptide modified with heptasaccharide glycan, plus 1, 2, 3, and 4 phosphate groups respectively and a variable numbers methyl groups. However, comparison shows the abundance of glycopeptides harbouring the longer chain glycans to be markedly reduced in the AH-3ΔWecP mutant. A list of ion intensities ratios (compared to wild type) for representative glycopeptides from each cluster for this peptide in the AH-3ΔWecP, are shown in Table 1. A similar pattern of glycosylation was observed with a second polar flagellin glycopeptide from FlaB, MTSFTISGIASSTK (Table 1, and Mass spectrometry analyses of polar flagellin from *A. hydrophila* AH-3 *gne* mutant section), with the presence of full length sugar chains modifying the polar flagellin, but at much reduced levels compared with wild type flagellin modification.

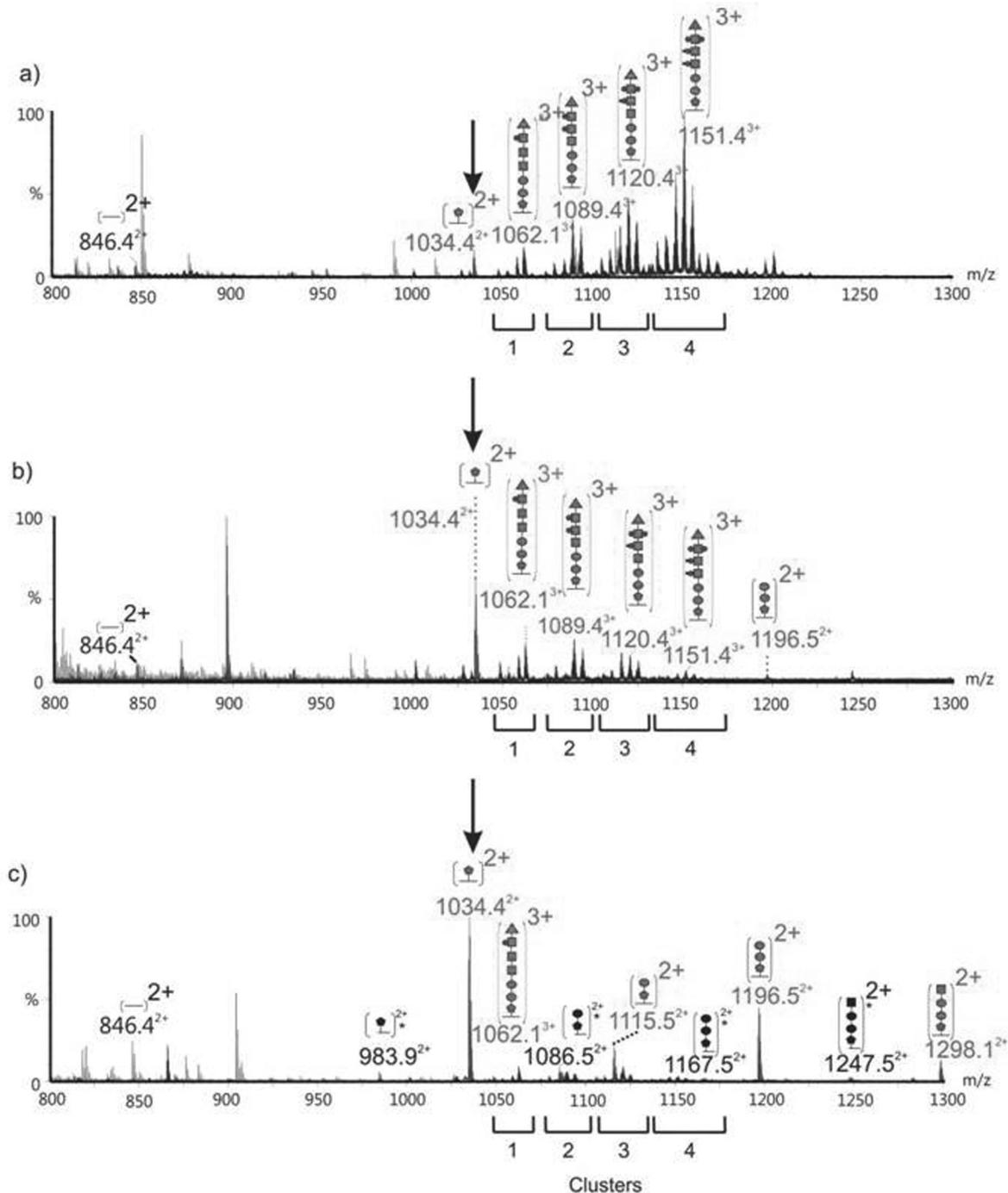
#### *A. hydrophila* AH-3 *gne* Mutant (AH-2767)

The AH-2767 mutant was still able to produce polar and lateral flagella but our previous work showed that the bacteria had a clear reduction in their motility [19] (Figure 1). In the current work, we examined the polar flagellum by EM and observed that it was shorter and more fragile in the AH-2767 mutant compared with wild type strain (Figure 4). The mutant was fully complemented by pACYC-GNE plasmid [19] and wild type polar flagellin restored, as could be observed in Figure 4.

We purified the polar flagellum from the mutant and compared it with the flagellum of the wild type strain. The amount of polar flagellin obtained from 11 culture of the mutant versus the same amount of wild type growth is reduced in approximately 70% judged by densitometry of the gel bands. Figure 4 shows that there is a large variability in the molecular weight of flagellins in the mutant, with bands corresponding to polar flagellin migrating to approximate molecular weights between 44 and 30 kDa. This is in comparison with polar flagellin from wild type, which migrates to three discrete bands between 43 and 45 kDa. A full recovery of the wild type polar flagellin profile and protein abundance was observed when the mutant was complemented by pACYC-GNE plasmid [19] (Figure 4b), and motility (Figure 1). No differences were observed between the wild type strain and the AH-2767 mutant in lateral flagella production when examined by EM or with purified lateral flagella.

#### Mass Spectrometry Analyses of Polar Flagellin from *A. hydrophila* AH-3 *gne* Mutant

Protein mass analysis was carried out on polar flagellin isolated from the AH-2767 mutant (AH-3 *gne* mutant). The MS profile showed a complex ion envelope with poor ionization, which could not be resolved to give observed intact protein masses. However, the protein MS spectrum did show an intense ion at  $m/z$  377 likely corresponding the glycan oxonium ion of the 376 Da pseudaminic acid derivative (data not shown). MS/MS analyses of tryptic peptides from polar flagellin isolated from the mutant showed four of the five glycopeptides previously observed in the wild type [9]. However, the predominant modification of these peptides in the mutant strain was observed to be a single 376 Da moiety, compared with the wild type flagellin where the major modification was a complex and variable heptasaccharide glycan chain. The MS/MS spectrum of the <sup>94–109</sup>TLAQQSANGSNNTDDR glycopeptide (sequence present in both FlaA and FlaB), with a 376 Da glycan modification is shown in Figure 5. Figure 3a and c, show the LC-MS spectra of flagellin tryptic digests from wild type and AH-2767 mutant at 13.1–13.8 minutes (elution time for the <sup>94–109</sup>TLAQQSANGSN NTDDR glycopeptide). Comparison of



**Figure 3. nLC-MS alignment of the AH-3 polar flagellin FlaA/FlaB glycopeptide.** The 1691 Da FlaA/FlaB peptide TLAQQSANGSNNTDDR (eluting between 13.1 and 13.8 minutes) was modified by a heptasaccharide glycan with HexNAc residues additionally variably modified by 0–2 phosphate and 0–2 methyl groups [9]. These additional variable modifications resulted in four major glycopeptide ion cluster regions, as indicated below each spectrum. The cluster number corresponds to the number of additional phosphate groups modifying the heptasaccharide, and peaks within that cluster possess a variable number of additional methyl groups. Only the most prominent peak within each cluster is annotated. a) Wild type polar flagellin. Glycoforms of the peptide modified with the heptasaccharide were more abundant, compared with the peptide modified with only a single 376 Da (this form of the glycopeptide is indicated in the Figure with an arrow at  $m/z$  1034.4). The glycopeptide peak intensity increased with the addition of each phosphate group. b) AH-3 $\Delta$ WecP mutant polar flagellin. In contrast to wild type, the predominant modification in AH-3 $\Delta$ WecP was a single 376 Da sugar. The glycopeptide clusters resulting from the heptasaccharide glycan and additional variable modification were observed, but with decreased intensity as compared to the monosaccharide modification. c) AH-2767 (*gnc* mutant) polar flagellin. A decrease in the complexity of glycan modification was observed. The most abundant modification observed was the single 376 Da glycan. Glycopeptide clusters were not observed in the same manner when compared to wild type and the longer chain modifying glycans were not observed. In addition, the unmodified peptide was also observed at  $m/z$  846.4<sup>2+</sup>. This was not detectable in wild type, Figure legend: solid pentagon = 376 Da sugar; ● = hexose; ■ = HexNAc; ▲ = 102 Da unknown moiety; ● = phosphorylation; ■ = methylation; \* = truncated peptide.  
doi:10.1371/journal.pone.0089630.g003

**Table 1.** Comparison of polar flagellin peptide and glycopeptide ion intensities between wild type and mutants.

Peptide Sequence (Peptide mass, Da)	Glycopeptide Cluster Region	Glycopeptide Ion ( <i>m/z</i> )	Charge State	Glycan Mass (Da)	Ion Intensity Ratio of mutant strain/Wild Type (WT)		
					WT	Gne <sup>a</sup>	ΔWecP <sup>a</sup>
<b>FlaA/FlaB<sup>(1)</sup></b>							
TLAQQSANGSNNTDDR (1690.8)	–	846.4	+2	0	1	7.47	0.74
	–	1034.4	+2	376	1	12.01	1.07
	1	1062.1	+3	1492	1	0.81	0.34
	2	1089.4	+3	1574	1	0.47*	0.34
	3	1120.4	+3	1667	1	0.35*	0.09
	4	1151.4	+3	1760	1	0.07*	0.03
<b>FlaB<sup>(2)</sup></b>							
MTSAFTISGIASSTK (1500.8)	–	751.5	+2	0	1	0.31	0.17
	–	939.4	+2	376	1	0.94	0.84
	1	998.7	+3	1492	1	0	0.69
	2	1026.1	+3	1574	1	0	0.18
	3	1057.1	+3	1667	1	0	0.06
	4	1088.1	+3	1760	1	0	0.02

<sup>a</sup>Gne corresponds to AH-2767 *gne* mutant and ΔWecP to AH-3ΔWecP mutant.

The relative intensity ratios for two polar flagellin peptides are shown: the peptide TLAQQSANGSNNTDDR peptide sequence common to both FlaA and FlaB (1690 Da) (1), while the peptide MTSFTISGIASSTK is present in FlaB only (1501 Da) (2). Unmodified forms of the peptides, peptides modified with the single 376 Da pseudaminic acid derivative, and representative glycopeptide ions from each ion cluster are listed. For each peptide/glycopeptide, the ion intensity expressed as a ratio relative to the ion intensity observed in wild type. Ion intensity ratios marked with an \* are approximate ratios where overlapping ions in that *m/z* region made it impossible to measure ion intensity due to a single ion.

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the MS spectra showed a much reduced intensity of the multiply charged ion clusters in the AH-2767 mutant strain. Almost no phosphorylation or methylation of the HexNAc residues was observed in the mutant strain. However, some heterogeneity was observed in the polar flagellin glycosylation in the AH-2767 mutant and this resulted from the presence of variable glycan chain lengths ranging from mono-saccharide to the full length heptasaccharide (annotated in Figure 3c). Specifically, the doubly charged ions at *m/z* 1034.4, 1115.5, 1196.5, and 1298.1 represent intermediate glycan chain lengths [Pse-162 or Pse-162–162 (162 = Hexose)] observed in the AH-2767 mutant but not in wild type. By comparing the relative intensity of the peaks with the wild type data, the relative intensity of the peaks it can be observed that AH-2767 mutant showed the most intense glycopeptide peak of doubly charged ion with *m/z* of 1034 (376 monosaccharide alone) and low intensity doubly charged glycopeptide ion peaks at *m/z* 1196 and 1115 (376 monosaccharide with two or one hexoses, respectively). Table 1 shows the relative intensities of the ion clusters for the polar flagellin from the mutant, compared with the wild type.

Figure 6 shows the LC-MS spectrum of a second glycopeptide, <sup>160–174</sup>MTSA FTISGIASSTK, which is unique to FlaB. As previously noted, the wild type polar flagellin (Figure 6a) shows a complex pattern of glycosylation, with glycan isoforms with varying degrees of phosphorylation and methylation, denoted in Figure 6a as clusters 1–4. Again, reduced complexity of glycosylation was observed in the polar flagellin AH-2767 mutant (Figure 6b), evidenced by the absence of the glycopeptide ion clusters. It is interesting to note that in the AH-2767 mutant, the unmodified form of the FlaB peptide (*m/z* 751.5) and the peptide modified only by the 376 Da moiety (*m/z* 939.4), were not observed at high levels, as shown in Figure 6 and Table 1. As previously indicated, AH-3ΔWecP polar flagellin showed reduced

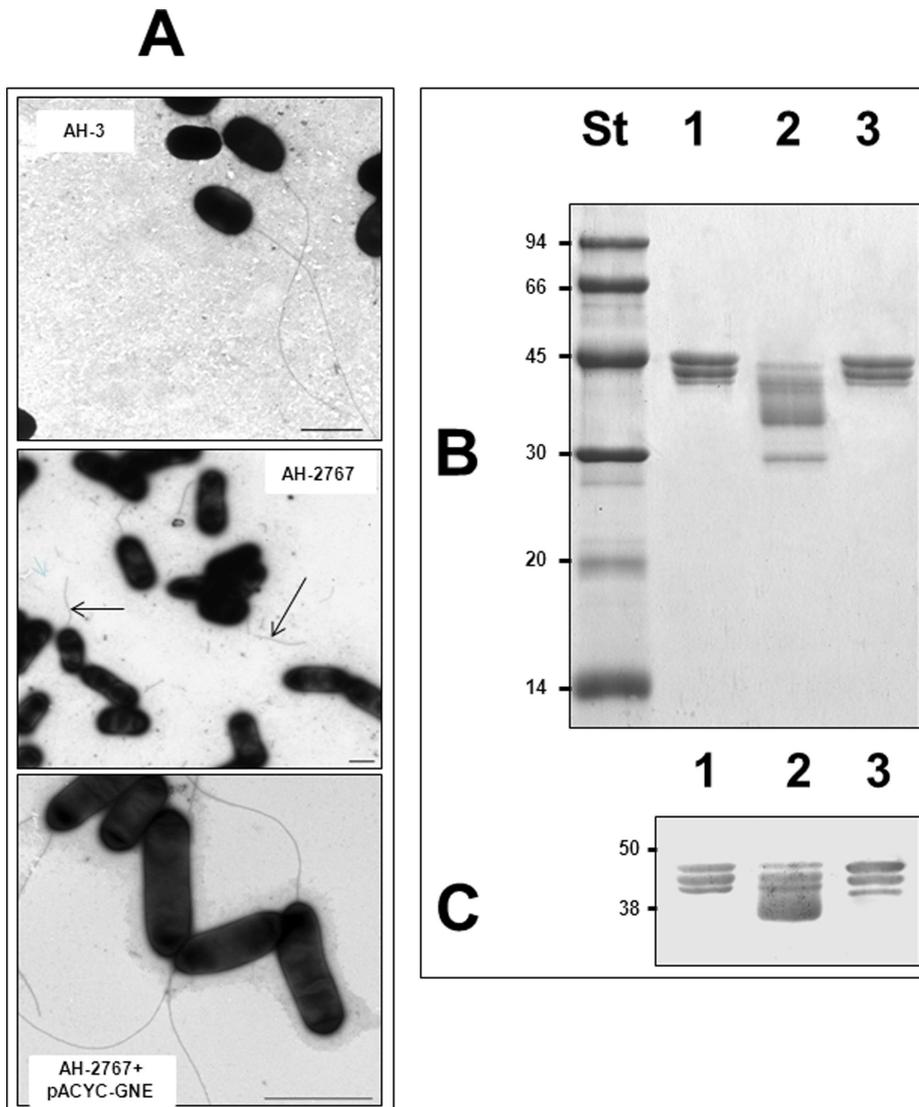
levels of full length sugar chains in comparison with the same flagellin from the wild type (Figure 6c).

Isolated polar flagellins from AH-2767 mutant were able to react with specific antiserum against GlcNAc while no reaction was observed with isolated polar flagellins from wild type strain or AH-3ΔWecP (Figure 4D).

### A. hydrophila AH-3 Mutants Lacking Only O34-antigen LPS

Both mutants (AH-2767 and AH-3ΔWecP) lack the O34-antigen LPS characteristic of this strain [20], and others have suggested the possible involvement of O-antigen LPS in flagella glycosylation in other bacteria [21]. We therefore investigated the possible role of O34-antigen LPS in *A. hydrophila* AH-3 flagella glycosylation.

Previously isolated mutants (AH-3ΔwaaL) [22] and AH-3ΔManC constructed in this study were also devoid of the O34-antigen LPS. AH-3ΔwaaL is able to produce O34-antigen LPS but lacks the O-antigen ligase (WaaL) that links it to the LPS-core. We have previously published a study using an insertional mutant in *manC* with possible polar effects in *wecP* of the cluster *wb<sub>034</sub>* [23]. Then, we generated in this study an in frame *manC* mutant in order to avoid polarity effects. AH-3ΔManC lacks the mannose-1-phosphate guanylyltransferase, required to produce GDP-Man, a biosynthetic precursor for polysaccharides. The AH-3ΔManC mutant is unable to produce O34-antigen LPS according to their LPS gel profile in SDS-PAGE (Figure 7A). No relevant differences in motility were observed in both mutants versus the wild type strain or by EM both mutants showed a similar polar flagellum as the wild type strain (Figure 7). Purified polar flagellins from both mutants showed the same molecular weight profile as wild type polar flagellins (Figure 8).



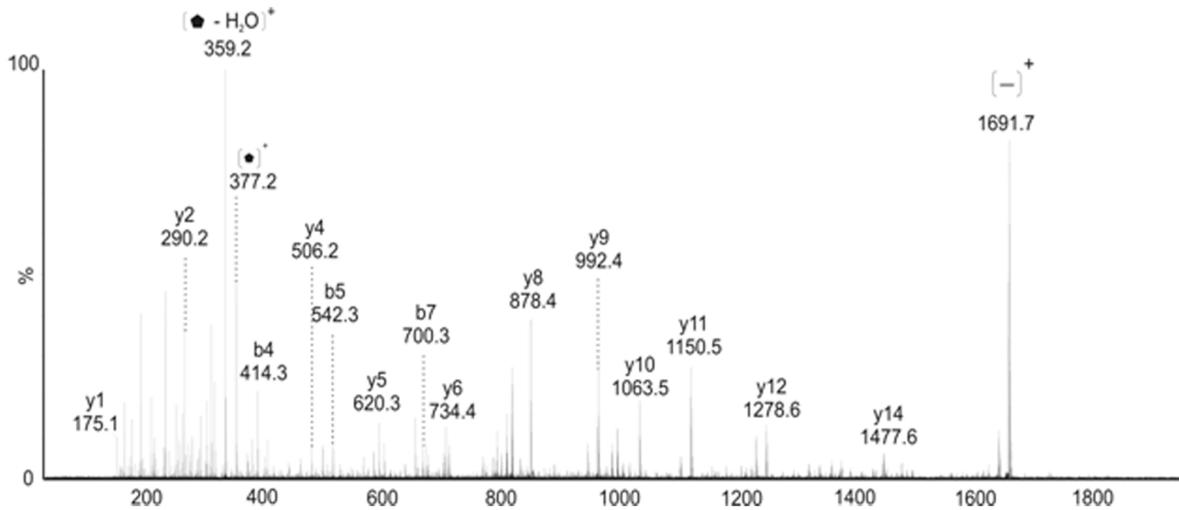
**Figure 4. A/Electron microscopy of whole cells from *A. hydrophila* strains stained according to Experimental Procedures.** Bar represents 1 μm. B/SDS-PAGE of purified polar flagellins. C/Western blot using specific antiserum against purified polar flagellins. St, size standard. 1, *A. hydrophila* AH-3 (wild type); 2, *A. hydrophila* AH-2767 *gnc* mutant; and 3, *A. hydrophila* AH-2767 mutant complemented with plasmid pACYC-GNE (19). D/Western blot using specific antiserum against GlcNAc. Lanes: 1, *A. hydrophila* AH-2767 *gnc* mutant; 2, *A. hydrophila* AH-3 (wild type); and 3, AH-3Δ*WecP* mutant. The arrows in 2A pointed out the more short and fragile flagellum of the mutant versus the wild type flagellum. doi:10.1371/journal.pone.0089630.g004

### A Second Lipid Carrier on Strain AH-3

The use of several primers able to amplify different Und-P domains in different *Aeromonas* strains allowed us to identify a second enzyme able to link sugars to a lipid carrier (named *WecX*: GenBank KF734980) in strain AH-3 (see Materials and Methods). This identification allowed us to obtain defined *wecX* insertion mutants devoid of it. The gene codifying for the enzyme *WecX* is located between a gene codifying for a signal transduction histidine kinase upstream and a two downstream genes codifying for glycosyltransferases which does not seem to be involved in LPS but maybe in exopolysaccharide production. Unfortunately, the complete genome of strain AH-3 is not currently available.

The single mutant AH-3:WecX was non motile (Figure 9) and unable to produce polar and lateral flagella by EM (Figure 10). The similar situation was observed for the double mutant AH-3Δ*WecP*:WecX. No changes could be observed in their LPS

profiles in comparison with their respective wild type in SDS-PAGE [18] (Figure 9). The complementation of the double mutant AH-3Δ*WecP*:WecX with pBAD-WecX was unable to change their LPS profile in gels (Figure 9). Because some unattached portions of flagella could be observed in the EM background of the mutants, we tried to purify the polar flagellin from the mutants by cesium chloride. A minor protein band was visualized on 1D-PAGE, obtained using 10 times more growth volume for flagellin purification from the mutants than the amount used for the wild type strain. Tandem mass spectrometry analyses of tryptic digests of the band showed it harbor low amounts of polar flagellin protein, with no detectable glycopeptides. Mass spectrometry analyses of the tryptic digests of this mutant gave 20 percent sequence coverage. De novo sequencing showed no evidence of previously observed glycopeptides, and no evidence of post translational modification of any peptides. Polar flagellin is



**Figure 5. nLC-MS/MS AH-2767 *gne* mutant polar flagellin glycopeptide spectrum.** nLC-MS/MS spectrum of the doubly charged ion at  $m/z$  1034.4 eluting between 13.1 and 13.8 minutes. The peptide sequence was identified by y and b ion series as  $^{94}\text{TLAQQSANGSNTDDR}^{109}$  which corresponds to both the FlaA and FlaB sequences. The unmodified singly charged peptide ion can be seen at  $m/z$  1691.7, giving a mass excess of 376 Da (pseudaminic acid derivative). The prominent peaks at  $m/z$  377 and 359 correspond to the glycan oxonium ion and its dehydrated form, respectively.

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synthesized in the cytoplasm fraction by these *wecX* mutants as the wild type, but very few if any are properly assembled in the membrane fraction when compared to the wild type (Figure 10).

When we introduced the pBAD-WecX into the single mutant AH-3:WecX or the double mutant AH-3 $\Delta$ WecP:WecX, and we grow the strains under inducing conditions (+0.2% arabinose), they recover the full motility (Figure 9) and the flagella production by EM was the same as observed with the wild type strain (Figure 10). The complemented strains showed flagellin in the membrane fraction and in purified flagella (Figure 10) with the same MW as the wild type. No changes in motility or flagella production by EM could be observed when we introduced the plasmid vector alone (pBAD33) and the mutant strains grow under inducing conditions.

The mutants that lack O34-antigen LPS showed a reduced virulence when tested in several animals by intraperitoneal injection [19,23]. When we tested the AH-3 $\Delta$ WecX or mutants unable to produce flagella from the same strain no such reduction of the virulence could be observed in the same animal models.

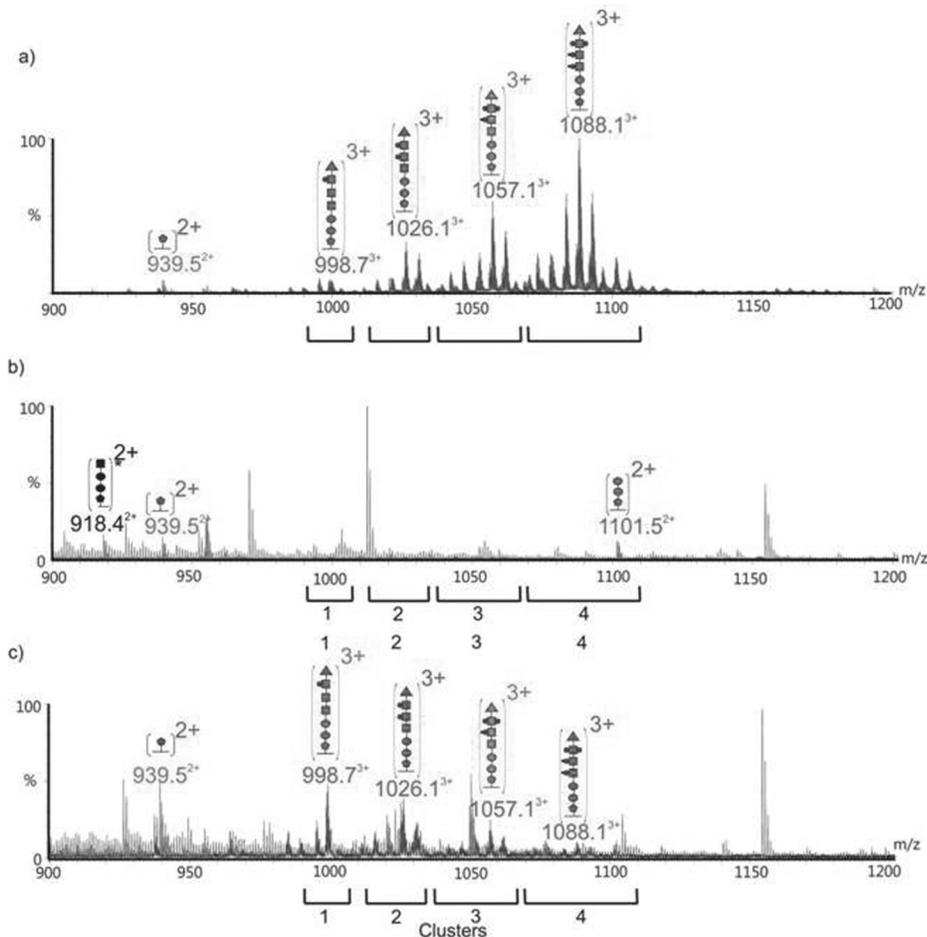
## Discussion

The list of bacterial species that modify their flagellin proteins with diverse glycans continues to grow and was recently reviewed [6,24], however an understanding of the biological role of glycosylation remains limited. In the current study, we show that flagellin glycosylation impacts the ability of *A. hydrophila* AH-3 to form full flagellar filaments and motility.

WecP is the integral membrane protein that catalyzes the transfer of GalNAc-1-phosphate onto Und-P and the major modification for AH-3 $\Delta$ WecP mutant was the loss of O34-antigen LPS [18]. Several fully sequenced strains of *Aeromonas* encode genes for more than enzyme linking sugars to a lipid carrier. For example, strain ATCC7966T [30] constitutively expresses polar flagellum and lacks an inducible lateral flagella [25], and showed several putative enzymes able to link sugars to lipid carriers in addition to WecP.

A second enzyme able to link sugars to a lipid carrier on strain AH-3 was identified in this study, denoted WecX, that we show is responsible for the heptasaccharide glycosylation of the polar flagellin without modifying the O34-antigen LPS. This conclusion is in agreement with the data of no changes in the LPS and no production of polar flagellum by EM, no motility, or the non-glycosylated flagellin observed in the mutants (AH-3:WecX and AH-3 $\Delta$ WecP:WecX). All these negative traits were recovered by the introduction of the AH-3 *wecX*. To our knowledge this is the first report of a lipid carrier involved in flagella O-glycosylation. It has been recently described that other external organelles like fimbriae showed O-glycosylation with the recruitment of a lipid carrier [10,26]. However, while fimbriae are inducible external organelles, the *A. hydrophila* AH-3 polar flagellum is constitutively expressed [27]. WecX protein sequence showed clear undecaprenyl-phosphate glucose phosphotransferase domain. Computer programs, such as TMHMM 2.0 (Prediction of transmembrane helices in proteins from the Center for Biological Sequence Analysis, Denmark; <http://www.cbs.dtu.dk/services/TMHMM/>), have been used to predict transmembrane helices and membrane topology models for proteins involved in the transfer of sugar phosphate residues to undecaprenol phosphate (Und-P) such as WecA [17], WecP [18] and WbaP [16]. The same computer program was used to model the *A. hydrophila* AH-3 WecX molecular topology revealing that not feed in any of the known models, but two clear transmembrane regions could be observed at the beginning (first 40 amino acid residues) and the end of the protein (the last 25 amino acid residues). It is important to notice that none of these transferase-catalyzed reactions to the membrane-associated polyprenol phosphate acceptor (Und-P) until now described [15] uses a sugar nucleotide related to Pse or a Pse derivative.

The results obtained in this current work allow us to suggest the hierarchy of polar flagellin O-glycosylation. While pseudaminic acid (Pse) biosynthetic mutants are unable to form flagella because they are unable to produce properly flagellin in the cytoplasm [9], the WecX mutant (AH-3:WecX) is able to do it. It seems unable to produce flagella probably because could not locate the heptasac-



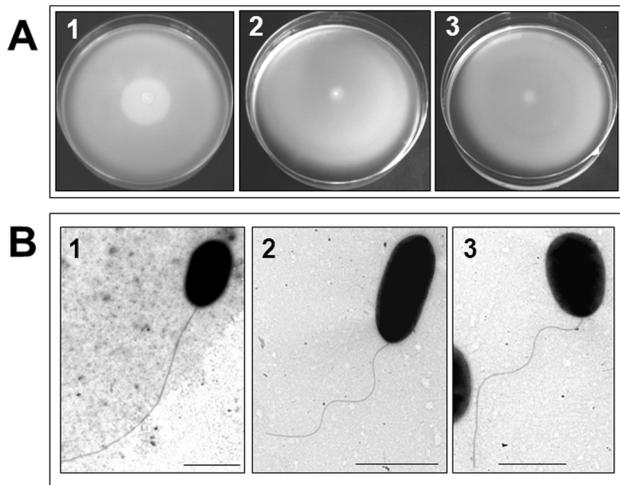
**Figure 6. nLC-MS alignment of AH-3 polar flagellin FlaB glycopeptide.** The 1501 Da FlaB peptide MTSFTISGASSTK (eluting between 17.9 and 18.9 minutes) was modified by the same heptasaccharide glycan with HexNAc residues additionally variably modified by phosphate and methyl groups [9]. These additional variable modifications resulted in four major glycopeptide ion cluster regions, as indicated below each spectrum. The cluster number corresponds to the number of additional phosphate groups modifying the heptasaccharide, and peaks within that cluster possess a variable number of additional methyl groups. Only the most prominent peak within each cluster is annotated. a) Wild type polar flagellin. The heptasaccharide modification was the most abundant form of modification, with only minor amounts of peptide harbouring the 376 Da sugar were observed. The glycopeptide peak intensity increases with the addition of each phosphate group to the glycans. b) AH-2767 *gne* mutant polar flagellin. In this mutant, the FlaB peptide showed only minor modification with intermediate glycan chains. The unmodified peptide and peptide modified only with the 376 Da sugar were also not observed at high levels. c) AH-3ΔWecP mutant polar flagellin. In contrast to wild type, the predominant modification in AH-3ΔWecP was a single 376 Da sugar. Clustering resulting from the heptasaccharide and additional variable modification similar to that observed in wild type polar flagellin was observed, but with decreased intensity as compared to the monosaccharide modification. Figure legend: solid pentagon = 376 Da sugar; ● = hexose; ■ = HexNAc; ▲ = 102 Da unknown moiety; ● = phosphorylation; ■ = methylation; \* = truncated peptide. doi:10.1371/journal.pone.0089630.g006

charide outside the membrane, absence of the lipid carrier. This second lipid carrier WecX is unable to restore the O:34 antigen LPS in the double mutant AH-3ΔWecP:WecX, thus indicating that is used only in flagella glycosylation.

Thus, the first initial sugar linked to the flagellin is Pse-like, with the hexasaccharide [(162-162-203-297-376-102 Da), 2 Hex, 3HexNAc unsubstituted or substituted with phosphate and methyl groups, and unknown glycan 102 Da], being this heptasaccharide produced by the lipid carrier WecX. We proposed the following molecular model (Figure 11). We suggest that WecX is able to link CMP-Pse-like to Und-P, and several different glycosyltransferases are able to form sequentially the heptasaccharide linked to Und-P, being first the glycosyltransferases that add Hex, then the glycosyltransferases that add HexNAc, and finally a putative transferase for the unknown glycan of 102

Da. Then, one enzyme that we named OTase like, transfers in an O-glycosylation basis these heptasaccharide to the threonine/serine amino acids of the polar flagellin. Once the flagellin molecules are glycosylated could be transported to produce the polar flagellum.

The *A. hydrophila* AH-2767 *gne* mutant showed a great reduction in the phenotypic traits (motility in swimming plates, polar flagellum by EM or molecular weight size variation) compared with the wild type strain. This is in agreement with the protein glycosylation data, which show the polar flagellin in this mutant to be modified with Pse or truncated glycan chains with one or two hexoses major moieties and only a little of the full length heptasaccharide moiety. The AH-2767 *gne* mutant is unable to form UPDGalNAc from UDPGlcNAc [19], suggesting that in the wild type, the HexNAc observed in the minimal amount of

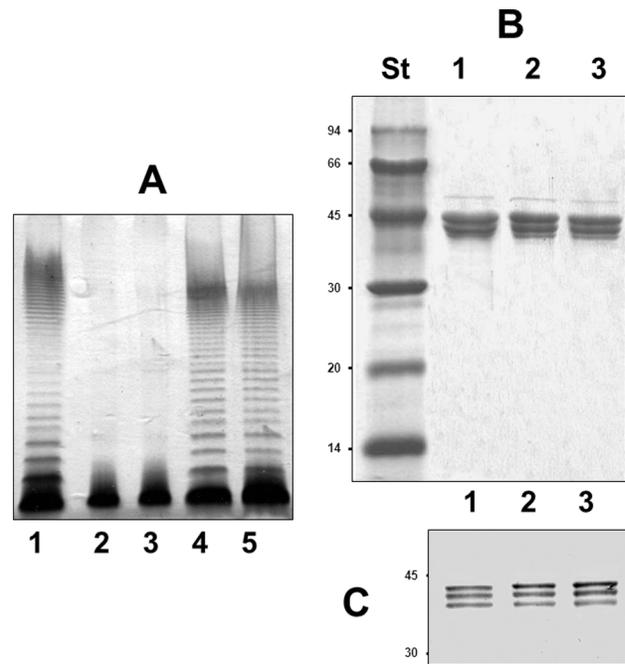


**Figure 7. A/Motility phenotypes exhibited in swim (0.25%) agar. B/Electron microscopy of whole cells from *A. hydrophila* strains stained according to Experimental Procedures. Bar represents 1 μm. 1, *A. hydrophila* AH-3 (wild type); 2, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔManC; 3, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔWaaL [22,23].**  
doi:10.1371/journal.pone.0089630.g007

heptasaccharide formed was GalNAc or a derivative of it. We could detect presence of GlcNAc in isolated AH-2767 *gne* mutant polar flagellins, which is not detected in the corresponding from the wild type, suggesting that this monosaccharide can be substituted into the glycan chain. This fact explains why the major glycosylation in the flagellin of this mutant is Pse, Pse-Hex or Pse-Hex-Hex. Although substitution of GlcNAc did not result in formation of wild type flagellin heptasaccharide glycosylation, a minimum amount could be detected in the mutant perhaps for the permissiveness of the corresponding glycosyl transferases. For instance *C. jejuni* PglA showed a relaxed specificity accepting several substrates in formation of the heptasaccharide for *N*-glycosylation [28,29].

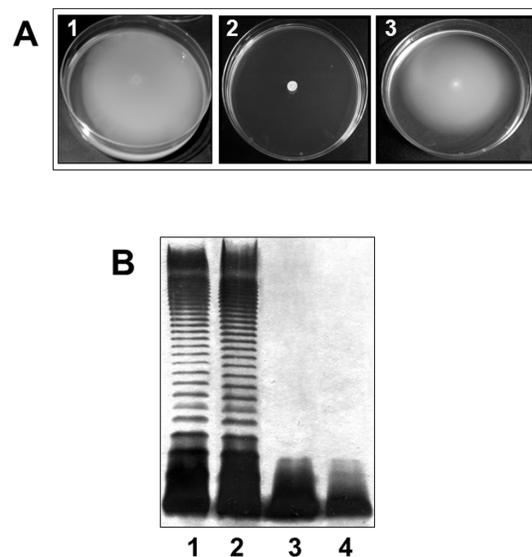
The AH-3ΔWecP mutant showed a slight reduction in motility or in the molecular weight of polar flagellins when compared to the wild type strain. In agreement, the major modification for AH-3ΔWecP polar flagellin was with a single 376 Da (Pse derivative) moiety and lower levels of the heptasaccharide. WecP could do a minor collaboration in flagellin glycosylation but it is not essential like WecX. Both mutants (AH-2767 *gne* and AH-3ΔWecP) are devoid of O34-antigen LPS [18,19]. O34-antigen LPS mutants (AH-3ΔManC and AH-3ΔwaaL) showed no changes in motility, flagella production, or molecular weight of the polar flagellin. From the glycosylation studies, we can conclude that the O34-antigen LPS is not involved in *A. hydrophila* AH-3 flagellin glycosylation, and the O34-antigen ligase (WaaL) is also not involved.

In several bacterial species, for example *C. jejuni* [30], *H. pylori* [31] and *C. difficile* [32], altered forms of flagellin glycosylation and neither mutant strain was able to form a complete wild type-like flagellum. In this study, abolished or incomplete flagellin glycosylation resulted in altered motility phenotypes. This was also observed with *C. difficile*, where abolition of flagellin glycosylation resulted in loss of motility [32]. In conclusion, the current study starts to unravel the complex mechanism of polar flagellar glycosylation in AH-3. We show for the first time the role of an Und-P carrier in flagellin modification with a proposed model (Figure 11), and determine the HexNAc modification to be

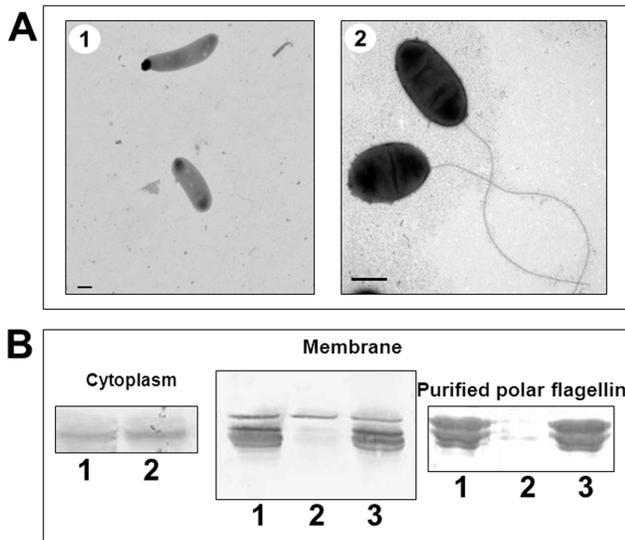


**Figure 8. Purified polar flagellins from several *A. hydrophila* strains obtained according to Materials and Methods. A, LPS profiles of 1, *A. hydrophila* AH-3 (wild type); 2, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔManC; 3, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔWaaL [22,23]; 4, AH-3ΔManC+pBAD-ManC and 5, AH-3ΔWaaL+pBAD-WaaL. B/SDS-PAGE and C/Western blot using specific antiserum against purified polar flagellins. St, size standard (14, 20, 30, 45, 60, and 94 kDa). 1, *A. hydrophila* AH-3 (wild type); 2, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔManC; and 3, *A. hydrophila* O<sup>-</sup> mutant AH-3ΔWaaL [22,23].**  
doi:10.1371/journal.pone.0089630.g008

GalNAc. In addition we have begun to shed light on the role of flagellum glycosylation in flagellum formation and motility.



**Figure 9. A/Motility phenotypes exhibited in swim (0.25%) agar by *A. hydrophila* AH-3 (1), AH-3:WecX mutant (2) and the mutant complemented with pBAD-WecX (3). B/LPS profiles of 1, *A. hydrophila* AH-3 (wild type); 2, AH-3:WecX mutant; 3, AH-3ΔWecP:WecX double mutant; and 4, AH-3ΔWecP:WecX with pBAD-WecX.**  
doi:10.1371/journal.pone.0089630.g009



**Figure 10. A/Electron microscopy of whole cells from *A. hydrophila* AH-3:WecX mutant (1) and the mutant complemented with pBAD-WecX (2) stained according to Experimental Procedures.** Bar represents 1µ. B/Western blots using specific antiserum against purified polar flagellins. Molecular weights are indicated. Cytoplasmic fractions (C), Whole membrane fractions (M), and partially purified polar flagellins (F), the fractions were separated as indicated in Materials and Methods section. Strains: 1, *A. hydrophila* AH-3 (wild type); 2, AH-3:WecX mutant, and 3 the mutant complemented with pBAD33-WecX.  
doi:10.1371/journal.pone.0089630.g010

**Materials and Methods**

**Bacterial Strains, Plasmids and Growth Conditions**

The bacterial strains and plasmids used in this study are listed in Table 2. *E. coli* strains were grown on Luria-Bertani (LB) Miller

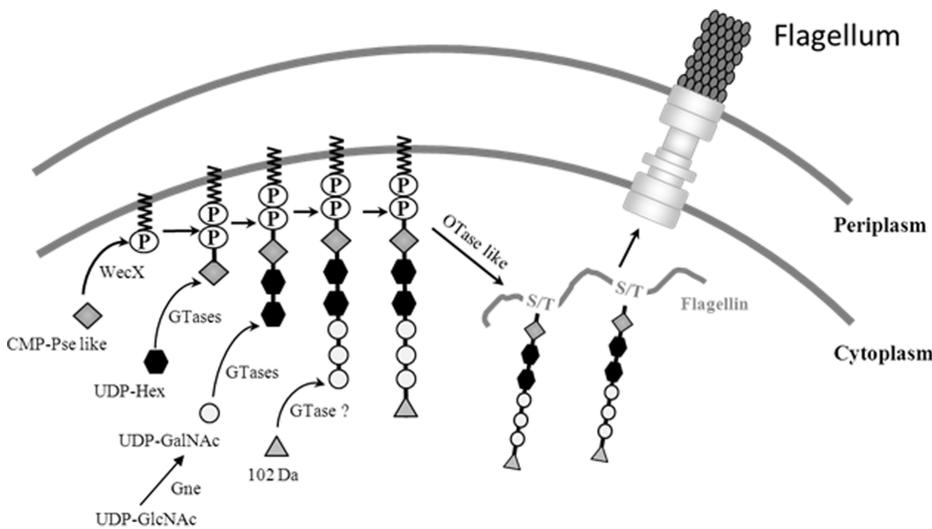
broth and LB Miller agar at 37ΔC, while *Aeromonas* strains were grown either in tryptic soy broth (TSB) or agar (TSA) at 30ΔC. When indicated kanamycin (50 µg/ml), rifampicin (100 µg/ml), spectinomycin (50 µg/ml), tetracycline (20 µg/ml) and chloramphenicol (25 µg/ml) were added to the media.

**DNA Techniques**

DNA manipulations were carried out essentially according to standard procedures [33]. DNA restriction endonucleases and *E. coli* DNA polymerase Klenow fragment were obtained from Promega. T4 DNA ligase and alkaline phosphatase were obtained from Invitrogen and GE Healthcare, respectively. PCR was performed using BioTaq DNA polymerase (Ecogen) in a Gene Amplifier PCR System 2400 Perkin Elmer Thermal Cycler. Plasmid DNA for sequencing was isolated by Qiagen plasmid purification kit (Qiagen, Inc. Ltd.) as recommended by the suppliers. Double-strand DNA sequencing was performed by using the Sanger dideoxy-chain termination method [34] with the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystem). Custom-designed primers used for DNA sequencing were purchased from Sigma-Aldrich. The DNA sequences were compared with those available in the GenBank and EMBL databases at the National Center for Biotechnology Information (NCBI) [35]. The Terminator search program in the GCG Wisconsin package was used to search for factor independent transcriptional terminators. The Neural Network Promoter Prediction, PromScan [36] and PRODORIC [37] were used to search promoter sequences.

**Construction of Defined Mutants**

The chromosomal in-frame *manC* deletion mutant *A. hydrophila* AH-3Δ*manC* was constructed by allelic exchange as described by Milton *et al.* [38]. Briefly, upstream (fragment AB) and downstream (fragment CD) of *manC* gene was independently amplified using two sets of asymmetric PCRs. Primer pairs A-ManC (5'-CGCGGATCCTTATTGTCAAGGGGACCTG-3') and B-



**Figure 11. Molecular model proposed for the polar flagellum glycosylation.** We suggest that WecX is able to link CMP-Pselike to Und-P, and several different glycosyltransferases are able to form sequentially the heptasaccharide linked to Und-P, being first the glycosyltransferases that add Hex (two of them), then the glycosyltransferases that add GalNAc or a derivate of it (three of them), and finally a putative transferase for the unknown glycan of 102 Da. Then an enzyme, that we named OTase like, transfers in O-glycosylation basis these heptasaccharide to the threonine/serine amino acids of the polar flagellin. Once the flagellins molecules are glycosylated could be transported to produce the polar flagellum. Gne is the enzyme that converts UDP-GlcNAc in UDP-GalNAc, and their lack jeopardizes the UDP-GalNAc formation.  
doi:10.1371/journal.pone.0089630.g011

**Table 2.** Bacterial strains and plasmids used.

Strain or plasmid	Relevant characteristics	Reference or source
<b>E. coli strains</b>		
DH5 $\alpha$	F <sup>-</sup> end A <i>hsdR17</i> (rK <sup>-</sup> mK <sup>+</sup> ) <i>supE44 thi-1 recA1 gyrA96 _80lacZM15</i>	[41]
XL1-Blue	<i>recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac</i> (F <sup>-</sup> <i>proABlacIqZ_M15 Tn10</i> )	Stratagene
S17-1	<i>hsdR pro recA</i> , RP4-2 in chromosomeKm::Tn7 (Tc::Mu)	[27]
BL21( $\lambda$ D3)	F <sup>-</sup> <i>ompT hsdS<sub>B</sub></i> (r <sub>B</sub> <sup>-</sup> m <sub>B</sub> <sup>-</sup> ) <i>gal dcm</i> ( $\lambda$ D3)	Novagen
<b>A. hydrophila strains</b>		
AH-3	O34, Wild type	[27]
AH-405	AH-3, spontaneous Rif <sup>R</sup>	[27]
AH-3 $\Delta$ ManC	AH-3 mutant in frame unable produce O34-antigen LPS	This study
AH-3 $\Delta$ PseB	AH-3 <i>pseB</i> mutant in frame with pDM4	[9]
AH-3 $\Delta$ PseB $\Delta$ ManC	AH-3 double mutant <i>pseB</i> and in frame unable produce O34-antigen LPS.	This study
AH-3:WecX	AH-3 <i>wecX</i> defined insertion mutant, Cm <sup>R</sup>	This study
AH-3 $\Delta$ WecP:WecX	AH-3 $\Delta$ WecP <i>wecX</i> defined insertion mutant, Cm <sup>R</sup>	This study
<b>Plasmids</b>		
pRK2073	Helper plasmid, Spc <sup>R</sup>	[27]
pCM100	Suicide plasmid, Cm <sup>R</sup>	[39]
pCM-WecX	pCM100 suicide plasmid with truncated <i>wecX</i> , Cm <sup>R</sup>	This study
pBAD33	arabinose inducible expression vector, Cm <sup>R</sup>	[40]
pBAD-ManC	pBAD33 with AH-3 <i>manC</i>	This study
pBAD-Waal	pBAD33 with AH-3 <i>waal</i>	[22]
pBAD-WecP	pBAD33 with AH-3 <i>wecP</i>	[18]
pBAD-WecX	pBAD33 with AH-3 <i>wecX</i>	This study
pACYC-GNE	pACYC184 with AH-3 <i>gne</i>	[19]
pDM4	<i>pir</i> dependent with <i>sacAB</i> genes, oriR6K, Cm <sup>R</sup>	[38]
pDM4-ManC	pDM4 with AH-3 <i>manC</i> fragment, Cm <sup>R</sup>	This study

doi:10.1371/journal.pone.0089630.t002

ManC (5'-CCCATCCAC TAAACTTAAACACTTTG-GAAAATGCTCACG-3') and C-ManC (5'-TGTTTAAAGTT-TAGTGGATGGGATTGAAATACGCTCCGGTA-3') and D-ManC (5'-CGCGGATCCTAACTGGGACCATCTCCTG-3') amplify DNA fragments of 830 (Man-AB) and 798 (Man-CD) bp for *manC* in-frame deletion. DNA fragments AB and CD were annealed at the overlapping regions (underlined letters in primers B and C) and amplified as a single fragment using primers A and D. The fusion products were purified, *Bam*HI digested (the *Bam*HI site is double-underlined in primer A and D), ligated into *Bgl*III-digested and phosphatase-treated pDM4 vector independently [38], electroporated into *E. coli* MC1061 ( $\lambda$ *pir*), and plated on chloramphenicol plates at 30°C to obtain pDM4-ManC plasmid. Plasmid pDM4-ManC with mutated gen were transferred into *A. hydrophila* AH-405 by triparental mating using the *E. coli* MC1061 ( $\lambda$ *pir*) containing the insertion constructs and the mobilizing strain HB101/pRK2073. Transconjugants were selected on plates containing chloramphenicol and rifampicin. PCR analysis confirmed that the vector had integrated correctly into the chromosomal DNA. After sucrose treatment, transconjugants that were rifampicin resistant (Rif<sup>R</sup>) and chloramphenicol sensitive (Cm<sup>S</sup>) were chosen and confirmed by PCR, being one of the AH-3 $\Delta$ ManC. Similar procedure was used to obtain the double mutant AH-3 $\Delta$ PseB $\Delta$ ManC by using plasmid pDM4-ManC and *A. hydrophila* AH-3 $\Delta$ pseB [9].

The primers used for *wecX* internal amplification were 5'-CAGACG ATGGTCAGATCC -3' and 5'-

GTCTCTCCCTGCTTACCC-3' resulting in an amplicon of 586 bp that was subcloned in pGEMT. After *Eco*RI digestion the plasmid pGEMT-*wecX* was treated with *E. coli* DNA polymerase I (Klenow fragment) to create blunt ends in order to ligate the band to pCM100 (suicide plasmid,  $\lambda$ *pir* dependent, [40]) to obtain plasmid pCM-WecX. This plasmid was used to isolate *wecX* deficient mutants from AH-3 and AH-3 $\Delta$ WecP (AH-3:WecX and AH-3 $\Delta$ WecP;WecX, respectively) by a single recombination event according to previously described procedures [39].

### Plasmid Constructions

Plasmid pBAD-ManC and pBAD-WecX containing the complete *manC* and *wecX* of *A. hydrophila* AH-3 under the arabinose promoter (p<sub>BAD</sub>) on pBAD33 [40] were obtained, respectively. Oligonucleotides 5'- TCCCCCGGGGAAGCGATGGTCT-GAATCAC-3' and 5'-CCCAAGCTTAAACG CAAAACACACATCA-3' generated a band of 1687 bp containing the *manC* gene. Oligonucleotides 5'- GCTCTAGACACAGGTGCCGT-GATAAG-3' and 5'- TCCCCCGGGCACTGGTCAACGGTCTCG-3' generated a band of 900 bp containing the *wecX* gene. The amplified bands were digested with *Sma*I and *Hind*III and ligated into *Sma*I and *Hind*III digested pBAD33 vector to construct the pBAD-ManC plasmid, or digested with *Sma*I and *Xba*I like pBAD33 vector to construct the pBAD-WecX plasmid. Both plasmids were independently introduced into the *E. coli* DH5 $\alpha$  [41] and sequenced.

## Flagella Purification

*A. hydrophila* AH-3 was grown in TSB for the polar flagellum purification. For the isolation of lateral flagella the strains were grown in TSA and plates washed with 100 mM Tris (pH = 7.8). Cells were in both cases collected by centrifugation at 5000×g, and suspended in the same Tris buffer. Flagella were removed from the cells by shearing in a vortex with a glass bar for 3–4 minutes, and then passing repetitively (minimum six times) through a syringe. Cells were removed by centrifugation at 8000×g for 30 minutes, and the supernatant centrifuged at 18000×g for 20 minutes. From the remaining supernatant the flagella were pelleted by ultracentrifugation at 100 000×g for 60 minutes, and resuspended in 100 mM Tris (pH = 7.8) plus 2mM EDTA buffer. This flagella enriched fraction was purified in a cesium chloride gradient by ultracentrifugation at 60 000×g for 48 hours. The band containing the flagella was collected, the cesium chloride removed by extensive dialysis against the same buffer (100mM Tris 2mM EDTA). Purified flagella were analyzed by SDS-PAGE or by glycosylation chemical studies.

## Cell Fractions

*A. hydrophila* cells grown in tryptic soy broth at 25°C were harvested by centrifugation (5000×g), washed with 20 mM MgCl<sub>2</sub> in 100 mM Tris buffer (pH = 8.0), and resuspended in the same cold buffer, and French press cell lysis was performed. The lysates were centrifuged at 5000×g to remove unbroken cells. After centrifugation at 4°C for 1 h at 115,000×g, the cytoplasmic fraction remained in the supernatant, whereas the whole membrane fraction was retained in the pellet.

## Immunological Methods

Western blot of purified flagella was performed as briefly described. After SDS-PAGE, immunoblotting was carried out by transfer to polyvinylidene fluoride membranes (Millipore Corp., Bedford, Mass.) at 1.3 A for 1 h in the buffer of Towbin *et al.* [42]. The membranes were then incubated sequentially with 1% bovine serum albumin, specific anti-polar flagellins polyclonal serum [27] (1:2000), alkaline phosphatase-labeled goat anti-rabbit immunoglobulin G, and 5-bromo-4-chloroindolylphosphate disodium-nitroblue tetrazolium. Incubations were carried out for 1 h, and washing steps with 0.05% Tween 20 in phosphate-buffered saline were included after each incubation step.

## Motility Assays (Swarming and Swimming)

Freshly grown bacterial colonies were transferred with a sterile toothpick into the centre of swarm agar (1% tryptone, 0.5% NaCl, 0.5% agar) or swim agar (1% tryptone, 0.5% NaCl, 0.25% agar). The plates were incubated face up for 16–24 h at 25°C and motility was assessed by examining the migration of bacteria through the agar from the centre towards the periphery of the

plate. Moreover, swimming motility was assessed by light microscopy observations in liquid media.

## Transmission Electron Microscopy (TEM)

Bacterial suspensions were placed on Formvar-coated grids and negative stained with a 2% solution of uranyl acetate pH 4.1. Preparations were observed on a Hitachi 600 transmission electron microscope.

## Electrospray Liquid Chromatography Mass Spectrometry

Mass spectrometry studies of intact flagellin proteins were carried out using 1–5 µg of protein, exactly as described previously [9]. Glycopeptides were mapped using tandem mass spectrometry methods, exactly as reported in our previous work [9]. Briefly, purified flagellins (50 to 200 ng) were digested over night with trypsin (Promega, Madison, WI) at a ratio of 30:1 (protein/enzyme, vol/vol) in 50 mM ammonium bicarbonate at 37°C. Protein digests were analyzed by nano-liquid chromatography NS/MS (nLC-MS/MS) using a Q-TOF Ultima Hybrid quadrupole time of flight MS (Waters, Milford, MA) [44]. Front end peptide separation was carried out using online nanoAcquity ultrahigh-pressure liquid chromatography system (Waters, Milford, MA) using previously detailed setup [9]. MS/MS spectra were acquired using data dependent mode or in targeted analyses on doubly, triply, and quadruply charged ions in collision induced dissociation (CID) mode. Unmodified peptides were identified using MASCOT (Matrix Science, London, UK) as described in our earlier work [43]. Glycopeptide MS/MS spectra were *de novo* sequenced, with peptide type y and b ions highlighted for confirmation of the peptide sequence.

## Statistical Analysis

Results are expressed as the means standard deviations (SD) of three to four experiments. Student's *t* test was used to compare mean values. Differences were considered significant when *P* values were <0.05.

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## Author Contributions

Conceived and designed the experiments: SM KMF SMT MW RM JMT. Performed the experiments: SM KMF SMT MW RM JMT. Analyzed the data: SM KMF SMT MW RM JMT. Contributed reagents/materials/analysis tools: SM KMF SMT MW RM JMT. Wrote the paper: SM KMF SMT MW RM JMT.

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